BLAST Basic Local Alignment Search Tool

-   Appendix C

Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

Protein Sequence (223 letters)

Results for: lcl|54117 None(223aa)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
      lcl|54117
Description
      None
Molecule type
      amino acid
Query Length
      223

Subject ID
      gi|6706916|gb|AAF25499.1|AF058942_3
Description
      spike glycoprotein [bovine coronavirus]
Molecule type
      amino acid
Subject Length
      1363
Program
      BLASTP 2.2.22+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Reference - compositional score matrix adjustment
Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.
Other reports: Search Summary [Taxonomy reports]

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Filter string	F
Genetic Code	1
Window Size	40

Karlin-Altschul statistics

Params	Ungapped	Gapped

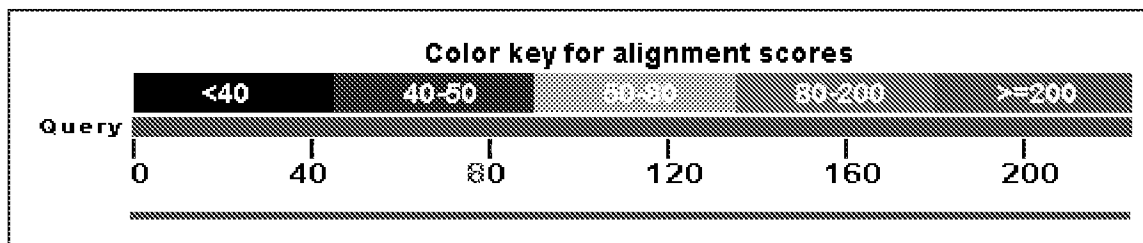| Lambda | 0.323458 | 0.267 |
| K | 0.140461 | 0.041 |
| H | 0.463759 | 0.14 |

Results Statistics

Effective search space 249664

Graphic Summary

Distribution of 5 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

Color key for alignment scores

| <40 | 40-50 | 50-80 | 80-200 | >=200 |

Query

```
0      40      80     120     160     200
```

Dot Matrix View

Plot of lcl|54117 vs gi|6706916|gb|AAF25499.1|AF058942_3 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

```
                                                              Score       E
Sequences producing significant alignments:                  (Bits)    Value

gb|AAF25499.1|AF058942_3   spike glycoprotein [bovine coronavirus]   436     7e-127
```

Alignments Select All Get selected sequences Distance tree of results Multiple alignment NEW

```
>gb|AAF25499.1|AF058942_3  spike glycoprotein [bovine coronavirus]
Length=1363

 Score =  436 bits (1122),  Expect = 7e-127, Method: Compositional matrix adjust.
 Identities = 220/223 (98%), Positives = 221/223 (99%), Gaps = 0/223 (0%)

Query  1     NHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFT  60
             NHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFT
Sbjct  1141  NHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFT  1200

Query  61    GSGYYYPEPITGNNVVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTLMAPD  120
             GSGYYYPEPITGNNVVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQT +APD
Sbjct  1201  GSGYYYPEPITGNNVVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAPD  1260

Query  121   LSLDYINVTFLDLQDEMNRLQEAIKVLNHSYINLKDIGTYEYYVKWPWYVWLLIGLAGVA  180
             LSLDYINVTFLDLQDEMNRLQEAIKVLN SYINLKDIGTYEYYVKWPWYVWLLIGLAGVA
Sbjct  1261  LSLDYINVTFLDLQDEMNRLQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGLAGVA  1320

Query  181   MLVLLFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIKTSHDD  223
             MLVLLFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIKTSHDD
Sbjct  1321  MLVLLFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIKTSHDD  1363


 Score = 23.1 bits (48),  Expect = 0.025, Method: Compositional matrix adjust.
 Identities = 16/62 (25%), Positives = 29/62 (46%), Gaps = 5/62 (8%)

Query  85    YTKAPDVMLNISTPNLPDFKEELDQWFKNQTLMAPDLSLDYINVTFLDLQDEMNRLQEAI  144
             YT  P   +      PNLPD   ++ W  ++++ +P    L++    TF +    M+ L  I
Sbjct  313   YTVQPIADVYRRIPNLPDCN--IEAWLNDKSVPSP---LNWERKTFSNCNFNMSSLMSFI  367

Query  145   KV  146
             +
Sbjct  368   QA  369


 Score = 20.8 bits (42),  Expect = 0.13, Method: Compositional matrix adjust.
 Identities = 9/30 (30%), Positives = 13/30 (43%), Gaps = 0/30 (0%)

Query  14    LYFIHFSYVPTKYVTAKVSPGLCIAGDRGI  43
             +Y  H     PT +   K+   LC+    GI
Sbjct  474   VYAQHCFKAPTNFCPCKLDGSLCVGSGSGI  503


 Score = 17.7 bits (34),  Expect = 1.2, Method: Compositional matrix adjust.
 Identities = 9/24 (37%), Positives = 12/24 (50%), Gaps = 0/24 (0%)

Query  34    GLCIAGDRGIAPKSGYFVNVNNTW  57
             G+C+  D      G FV VN T+
Sbjct  629   GVCVNYDLYGITGQGIFVEVNATY  652
```

```
Score = 17.3 bits (33),  Expect = 1.4, Method: Compositional matrix adjust.
Identities = 7/24 (29%), Positives = 14/24 (58%), Gaps = 0/24 (0%)

Query  55    NTWMFTGSGYYYPEPITGNNVVVM  78
             N ++ T   +YY  P+T N+ + +
Sbjct  235   NVYLGTVLSHYYVMPLTCNSAMTL  258
```

Select All Get selected sequences Distance tree of results Multiple alignment NEW